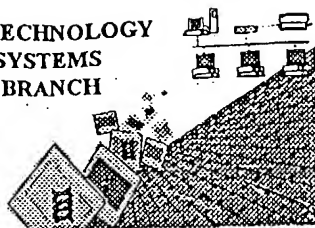# RAW SEQUENCE LISTING
·ERROR REPORT

The. Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/789,494A*

Source: *1Fwo*

Date Processed by STIC: *11/10/04*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

   http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
   U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/789,494A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

·2____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.

4 ✓ Non-ASCII — The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5____ Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) ... SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.

11____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

RAW SEQUENCE LISTING   DATE: 11/10/2004
PATENT APPLICATION: US/10/789,494A   TIME: 16:20:14

Input Set : A:\PTO.FG.txt
Output Set: N:\CRF4\11102004\J789494A.raw

see item 4 on Error Summary Sheet

```
  2 <110> APPLICANT: TSUBOUCHI, Kozo
  3         YAMADA, Hiromi
  5 <120> TITLE OF INVENTION: EXTRACTION AND UTILIZATION OF CELL
  6         GROWTH-PROMOTING PEPTIDES FROM SILK PROTEIN
  8 <130> FILE REFERENCE: OPS 635
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/789,494A
 11 <141> CURRENT FILING DATE: 2004-02-27
 13 <150> PRIOR APPLICATION NUMBER: JP 2003-55048
 14 <151> PRIOR FILING DATE: 2003-02-28
 16 <160> NUMBER OF SEQ ID NOS: 85
```

pp 1-2-3 *Does Not Comply Corrected Diskette Needed*

ERRORED SEQUENCES

```
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 10
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Bombyx mori
 23 <220> FEATURE:      delete <220> if no <221>, <222>, or <223> is shown
 25 <400> SEQUENCE: 1
 26 Val Ile Thr Thr Asp Ser Asp Gly Asn Glu
E--> 27    5      10     5          misaligned numbers. See item 3 on Error Summary Sheet.
 29 <210> SEQ ID NO: 2
 30 <211> LENGTH: 8
 31 <212> TYPE: PRT
 32 <213> ORGANISM: Bombyx mori
 34 <220> FEATURE:
 36 <400> SEQUENCE: 2
 37 Asn Ile Asn Asp Phe Asp Glu Asp
E--> 38    5         5          same error
 78 <210> SEQ ID NO: 6
 79 <211> LENGTH: 6
 80 <212> TYPE: PRT
 81 <213> ORGANISM: Antheraea yamamai
 83 <220> FEATURE:
 85 <400> SEQUENCE: 6
 86 Asp Glu Tyr Val Asp Asn
E--> 87    5                   same
102 <210> SEQ ID NO: 8
103 <211> LENGTH: 13
104 <212> TYPE: PRT
105 <213> ORGANISM: Antheraea yamamai
107 <220> FEATURE:
```

RAW SEQUENCE LISTING   DATE: 11/10/2004
PATENT APPLICATION: US/10/789,494A   TIME: 16:20:14

Input Set : A:\PTO.FG.txt
Output Set: N:\CRF4\11102004\J789494A.raw

```
109 <400> SEQUENCE: 8
110 Asp Asp Gly Phe Val Leu Asp Gly Gly Tyr    same
111    5    10
112 Asp Ser Glu
693 <210> SEQ ID NO: 47
694 <211> LENGTH: 15  /6 shown below
695 <212> TYPE: PRT
696 <213> ORGANISM: Antheraea yamamai
698 <220> FEATURE:
700 <400> SEQUENCE: 47
701 Ser Gly Ala Gly Gly Ser Gly Gly Tyr Gly Gly Tyr Gly Ser
702                5                    10
703 Asp Ser
704 15
```

16th amino acid

<210> 1
<211> 10
<212> PRT
<213> Bombyx mori

do not use italics

Per Sequence Rules, use a fixed-width font

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

```
L:10   M:270 C: Current Application Number differs, Replaced Current Application Number
L:27   M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:38   M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:87   M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:111  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:704  M:252 E: No. of Seq. differs, <211> LENGTH:Input:15 Found:16 SEQ:47
L:1163 M:283 W: Missing Blank Line separator, <400> field identifier
```